

141287

STIC-Biotech/ChemLib

From: Romeo, David
Sent: Monday, December 27, 2004 6:24 PM
To: STIC-Biotech/ChemLib
Subject: 10014162

Requester's Name: ... David Romeo
Serial Number: ... 10014162
Art Unit: ... 1647
Office: ... REM 4D39
Mailbox: ... REM 4C70
Phone: ... 571 272-0890
Date of Request: ... 12/27/2004

PLEASE PROVIDE RESULTS ON DISK(s)

Search the commercial/public and interference files for SEQ ID NO: 1.

STAFF USE ONLY

Searcher: HART
Searcher Phone: 2-
Date Searcher Picked up: 12/29/04
Date Completed: 1/3/05
Searcher Prep/Rev. Time: 8
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # 1 _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 1001 _____
WWW/Internet: _____
Other(Specify): _____

OM protein - protein search, using sw model

Run on: December 29, 2004, 15:22:36 ; Search time 156 Seconds
(without alignments)
89.682 Million cell updates/sec

Title: US-10-014-162-1
Perfect score: 196
Sequence: 1 SLALDDAAFRERARLLAALERRHWNLSYMKLLVLDAP 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980a:*
2: Geneseqp1990a:*
3: Geneseqp2000a:*
4: Geneseqp2001a:*
5: Geneseqp2002a:*
6: Geneseqp2003a:*
7: Geneseqp2003ba:*
8: Geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	ID	Description
1	196	100.0	39 4 AAB80490	Aab80490 PTH2 rece
2	196	100.0	39 5 AAE23970	Aae23970 Human TIP
3	196	100.0	39 5 ABB82202	Abb82202 TIF39 pol
4	196	100.0	39 6 ABP56764	Abp56764 Human TIP
5	196	100.0	40 5 AAU73181	Aau73181 Parathyro
6	196	100.0	100 5 AAE23969	Aae23969 Human TIP
7	196	100.0	100 5 ABB82210	Abb82210 Human TIP
8	196	100.0	100 6 ABP56763	Abp56763 Human TIP
9	192	98.0	38 4 AAB80489	Aab80489 PTH2 rece
10	189	96.4	38 4 AAB80526	Aab80526 PTH2 rece
11	188	95.9	37 4 AAB80488	Aab80488 PTH2 rece
12	188	95.9	37 5 ABB82197	Abb82197 TIF39 trn
13	185	94.4	37 4 AAB80525	Aab80525 PTH2 rece
14	184	93.9	36 4 AAB80487	Aab80487 PTH2 rece
15	184	91.8	35 4 AAB80527	Aab80527 PTH2 rece
16	180	91.3	35 4 AAB80486	Aab80486 PTH2 rece
17	179	89.8	34 4 AAB80524	Aab80524 PTH2 rece
18	176	89.8	34 4 AAB80528	Aab80528 PTH2 rece
19	176	89.3	35 4 AAB80485	Aab80485 PTH2 rece
20	175	87.8	100 5 ABB82211	Abb82211 Mouse TIP
21	172	87.8	100 5 ABB82211	Abb82211 Mouse TIP

22	172	87.8	100 6 ABP56765	Abp56765 Mouse TIP
23	171	87.2	34 4 AAB80522	Aab80522 PTH2 rece
24	170	86.7	33 4 AAB80484	Aab80484 PTH2 rece
25	170	86.7	33 4 AAB80529	Aab80529 PTH2 rece
26	167	85.2	33 4 AAB80521	Aab80521 PTH2 rece
27	164	83.7	32 4 AAB80483	Aab80483 PTH2 rece
28	164	83.7	32 4 AAB80530	Aab80530 PTH2 rece
29	164	83.7	32 5 ABB82198	Abb82198 TIF39 trn
30	163	83.2	32 4 AAB80520	Aab80520 PTH2 rece
31	160	81.6	31 4 AAB80482	Aab80482 PTH2 rece
32	160	81.6	31 4 AAB80531	Aab80531 PTH2 rece
33	160	81.6	31 5 ABB82196	Abb82196 TIF39 trn
34	158	80.6	31 4 AAB80519	Aab80519 PTH2 rece
35	156	79.6	30 4 AAB80481	Aab80481 PTH2 rece
36	156	79.6	30 4 AAB80532	Aab80532 PTH2 rece
37	156	79.6	30 5 ABB82199	Abb82199 TIF39 trn
38	150	76.5	29 4 AAB80480	Aab80480 PTH2 rece
39	150	76.5	29 4 AAB80533	Aab80533 TIF39 trn
40	150	76.5	29 5 ABB82200	Abb82200 PTH2 rece
41	150	76.5	30 4 AAB80518	Aab80518 PTH2 rece
42	150	76.5	37 5 ABB82208	Abb82208 ChimERIC
43	145	74.0	28 4 AAB80479	Aab80479 PTH2 rece
44	145	74.0	28 4 AAB80534	Aab80534 PTH2 rece
45	145	74.0	28 5 ABB82201	Abb82201 TIF39 trn

ALIGNMENTS

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 15:03:39 ; Search time 37 Seconds
(without alignments)
69.903 Million cell updates/sec

Title: US-10-014-162-1
Perfect score: 196
Sequence: 1 SLALDDAAFRERARLLAALERRHWNLSYMKLLVLDAP 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTU2.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	196	100.0	39	4	US-09-843-221A-160
2	196	100.0	39	4	US-09-843-221A-170
3	58	29.6	651	4	US-09-252-991A-18065
4	57	29.1	216	4	US-09-252-991A-26519
5	55.5	28.3	736	3	US-09-738-884-2
6	55.5	28.3	736	3	US-09-800-971-2
7	55.5	28.3	736	3	US-10-096-961A-2
8	55	28.1	6095	3	US-09-144-085-2
9	53	27.0	248	4	US-09-248-796A-15408
10	52	26.5	252	4	US-09-489-039A-12324
11	52	26.5	679	4	US-09-252-991A-28325
12	52	26.5	733	4	US-09-434-408-2
13	51	26.0	304	4	US-09-543-681A-4631
14	50.5	25.8	221	4	US-09-489-039A-10862
15	50	25.5	138	4	US-09-489-039A-10201
16	50	25.5	254	4	US-09-248-796A-16421
17	50	25.5	315	4	US-09-134-000C-6449
18	50	25.5	323	4	US-09-489-039A-12436
19	50	25.5	583	4	US-09-252-991A-32735
20	50	25.5	718	4	US-09-252-991A-28229
21	49.5	25.3	563	4	US-08-111-731A-142
22	49.5	25.3	850	4	US-09-904-389-2
23	49	25.0	48	6	5168045-6
24	49	25.0	48	6	5182364-14
25	49	25.0	142	4	US-09-489-039A-8648
26	49	25.0	372	4	US-10-265-012-14
27	49	25.0	434	4	US-10-265-012-10
28	49	25.0	507	4	US-10-265-012-12
29	49	25.0	569	4	US-10-265-012-8
30	49	25.0	608	4	US-10-265-012-2
31	49	25.0	679	4	US-09-252-991A-25400
32	49	25.0	875	4	US-09-252-991A-30056
33	48.5	24.7	280	4	US-09-540-236-2047
34	48.5	24.7	456	4	US-09-489-039A-10363
35	48	24.5	100	4	US-09-621-976-5948
36	48	24.5	265	4	US-09-489-039A-10393
37	48	24.5	478	4	US-09-489-039A-12483
38	48	24.5	599	4	US-09-489-039A-12768
39	48	24.5	1093	4	US-09-248-796A-17108
40	47.5	24.2	170	4	US-09-252-991A-24411
41	47.5	24.2	320	4	US-09-252-991A-30676
42	47.5	24.2	369	4	US-09-252-991A-24959
43	47	24.0	110	4	US-09-270-767-32515
44	47	24.0	110	4	US-09-270-767-47732
45	47	24.0	158	4	US-09-252-991A-20822

ALIGNMENTS
GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: December 29, 2004, 15:12:10 ; Search time 144 Seconds
(without alignments)
97.426 Million cell updates/sec

Title: US-10-014-162-1
Perfect score: 196
Sequence: 1 STALDDAARFRRARLALALRRHWLNSYMKLVLDPAD 39
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:	1599051 seqs, 359727711 residues	1599051
Total number of hits satisfying chosen parameters:		
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0 % Maximum Match 100 % Listing first 45 summaries	
Database :	Published Applications: AA:*	
1:	/cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*	
2:	/cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep:*	
3:	/cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*	
4:	/cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*	
5:	/cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.pep:*	
6:	/cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep:*	
7:	/cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*	
8:	/cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*	
9:	/cgn2_6/ptodata/2/pubppa/US09A_PUBCOMB.pep:*	
10:	/cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep:*	
11:	/cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep:*	
12:	/cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*	
13:	/cgn2_6/ptodata/2/pubppa/US10B_PUBCOMB.pep:*	
14:	/cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*	
15:	/cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep:*	
16:	/cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep:*	
17:	/cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep:*	
18:	/cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*	
19:	/cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*	
20:	/cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	196	100.0	39	10	US-09-843-221A-160
2	196	100.0	39	10	US-09-843-221A-170
3	196	100.0	39	14	US-10-014-162-1
4	196	100.0	39	16	US-10-399-602-12
5	196	100.0	39	16	US-10-399-602-14
6	196	100.0	39	16	US-10-466-483A-7
7	196	100.0	39	17	US-10-839-037-160
8	196	100.0	39	17	US-10-839-037-170
9	196	100.0	100	16	US-10-399-602-2
10	196	100.0	100	16	US-10-466-483A-31
11	192	98.0	38	14	US-10-014-162-2
12	189	96.4	38	14	US-10-014-162-38
13	188	95.9	37	14	US-10-014-162-3
14	188	95.9	37	16	US-10-466-483A-2
15	185	94.4	37	14	US-10-014-162-39
16	184	93.9	36	14	US-10-014-162-4
17	180	91.8	35	14	US-10-014-162-5
18	179	91.3	36	14	US-10-014-162-40
19	176	89.8	34	14	US-10-014-162-6
20	175	89.3	35	14	US-10-014-162-41
21	172	87.8	39	16	US-10-399-602-11
22	172	87.8	39	16	US-10-399-602-13
23	172	87.8	100	16	US-10-399-602-3
24	172	87.8	100	16	US-10-466-483A-32
25	171	87.2	34	14	US-10-014-162-42

25	170	86.7	33	14	US-10-014-162-7	Sequence 7, Appl
27	170	86.7	33	17	US-10-428-377-23	Sequence 23, Appl
28	170	86.7	33	17	US-10-428-377-27	Sequence 27, Appl
29	167	85.2	33	14	US-10-014-162-43	Sequence 43, Appl
30	164	83.7	32	14	US-10-014-162-8	Sequence 8, Appl
31	164	83.7	32	16	US-10-466-483A-3	Sequence 3, Appl
32	164	83.7	33	17	US-10-428-377-26	Sequence 44, Appl
33	163	83.2	32	14	US-10-014-162-44	Sequence 4, Appl
34	160	81.6	31	14	US-10-014-162-9	Sequence 9, Appl
35	160	81.6	31	14	US-10-014-162-78	Sequence 78, Appl
36	160	81.6	31	16	US-10-466-483A-1	Sequence 45, Appl
37	158	80.6	31	14	US-10-014-162-45	Sequence 10, Appl
38	156	79.6	30	14	US-10-014-162-10	Sequence 79, Appl
39	156	79.6	30	14	US-10-014-162-79	Sequence 4, Appl
40	156	79.6	30	16	US-10-466-483A-4	Sequence 11, Appl
41	150	76.5	29	14	US-10-014-162-11	Sequence 80, Appl
42	150	76.5	29	14	US-10-014-162-80	Sequence 5, Appl
43	150	76.5	29	16	US-10-466-483A-5	Sequence 46, Appl
44	150	76.5	30	14	US-10-014-162-46	Sequence 13, Appl
45	150	76.5	37	16	US-10-466-483A-13	

ALIGNMENTS
GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 15:02:54 ; Search time 468 Seconds
(without alignments)
92.333 Million cell updates/sec

Title: US-10-014-162-1
Perfect score: 196
Sequence: 1 STATADAAFRERARLALALERRRWLWNSYMKLVLDAP 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:
1: /cgn2_6/ptodata/1/paa/PCUS.COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06.COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07.COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08.COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081.COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US082.COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083.COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US084.COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US085.COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US087.COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US088.COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US089.COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US090.COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US091.COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US092.COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US092.COMB.pep:*

17: /cgn2_6/ptodata/1/paa/US094.COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US095.COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US096.COMB.pep:*
20: /cgn2_6/ptodata/1/paa/US097A.COMB.pep:*
21: /cgn2_6/ptodata/1/paa/US097B.COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US098.COMB.pep:*
23: /cgn2_6/ptodata/1/paa/US099A.COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US099B.COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US100.COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US101.COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US102.COMB.pep:*
28: /cgn2_6/ptodata/1/paa/US103.COMB.pep:*
29: /cgn2_6/ptodata/1/paa/US104.COMB.pep:*
30: /cgn2_6/ptodata/1/paa/US105.COMB.pep:*
31: /cgn2_6/ptodata/1/paa/US106.COMB.pep:*
32: /cgn2_6/ptodata/1/paa/US107.COMB.pep:*
33: /cgn2_6/ptodata/1/paa/US108.COMB.pep:*
34: /cgn2_6/ptodata/1/paa/US109.COMB.pep:*
35: /cgn2_6/ptodata/1/paa/US109.COMB.pep:*
36: /cgn2_6/ptodata/1/paa/US109.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB	ID	Description
1	196	100.0	39	1	PCT-US01-31954-12	Sequence 12, Appl
2	196	100.0	39	1	PCT-US01-31954-14	Sequence 14, Appl
3	196	100.0	39	1	PCT-US02-01183-7	Sequence 7, Appl
4	196	100.0	39	1	PCT-US02-18771-3	Sequence 3, Appl
5	196	100.0	39	26	US-10-014-162-1	Sequence 1, Appl
6	196	100.0	39	29	US-10-399-602-12	Sequence 12, Appl
7	196	100.0	39	29	US-10-399-602-14	Sequence 14, Appl
8	196	100.0	39	30	US-10-466-483A-7	Sequence 160, App
9	196	100.0	39	34	US-10-839-037-160	Sequence 170, App
10	196	100.0	39	34	US-10-839-037-170	Sequence 7, Appl
11	196	100.0	39	36	US-60-261-804-7	Sequence 2, Appl
12	196	100.0	100	1	PCT-US01-31954-2	Sequence 31, Appl
13	196	100.0	100	1	PCT-US02-18771-2	Sequence 2, Appl
14	196	100.0	100	29	US-10-399-602-2	Sequence 31, Appl
15	196	100.0	100	30	US-10-466-483A-31	Sequence 38, Appl
16	196	100.0	100	26	US-10-014-162-2	Sequence 2, Appl
17	192	98.0	38	26	US-10-014-162-38	Sequence 2, Appl
18	189	96.4	37	26	PCT-US02-01183-2	Sequence 2, Appl
19	188	95.9	37	26	US-10-014-162-3	Sequence 3, Appl
20	188	95.9	37	26	US-10-014-162-3	Sequence 3, Appl
21	188	95.9	37	36	US-60-261-804-2	Sequence 39, Appl
22	188	95.9	37	36	US-60-261-804-2	Sequence 39, Appl
23	185	94.4	37	26	US-10-014-162-4	Sequence 4, Appl
24	184	93.9	36	26	US-10-014-162-5	Sequence 4, Appl
25	180	91.8	36	26	US-10-014-162-5	Sequence 4, Appl
26	179	91.3	36	26	US-10-014-162-40	Sequence 4, Appl
27	176	89.8	34	26	US-10-014-162-6	Sequence 41, Appl
28	175	89.3	35	26	US-10-014-162-41	Sequence 11, Appl
29	172	87.8	39	1	PCT-US01-31954-11	Sequence 13, Appl
30	172	87.8	39	29	US-10-399-602-11	Sequence 13, Appl
31	172	87.8	39	29	US-10-399-602-13	Sequence 13, Appl
32	172	87.8	39	29	PCT-US01-31954-3	Sequence 32, Appl
33	172	87.8	100	1	PCT-US02-01183-32	Sequence 32, Appl
34	172	87.8	100	1	PCT-US02-18771-4	Sequence 32, Appl
35	172	87.8	100	29	US-10-399-602-3	Sequence 32, Appl
36	172	87.8	100	30	US-10-466-483A-32	Sequence 32, Appl
37	172	87.8	100	33	US-10-712-124-72	Sequence 72, Appl
38	172	87.8	100	33	US-10-712-124-72	Sequence 72, Appl

39	171	87.2	34	26	US-10-014-162-42	Sequence 42, Appl
40	170	86.7	33	1	PCT-US04-13723-23	Sequence 23, Appl
41	170	86.7	33	1	PCT-US04-13723-27	Sequence 27, Appl
42	170	86.7	33	26	US-10-014-162-7	Sequence 7, Appl
43	170	86.7	33	30	US-10-428-377-23	Sequence 23, Appl
44	170	86.7	33	30	US-10-428-377-27	Sequence 27, Appl
45	167	85.2	33	26	US-10-014-162-43	Sequence 43, Appl

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 15:11:45 ; Search time 25 Seconds
(without alignments)
72.768 Million cell updates/sec

Title: US-10-014-162-1

Perfect score: 196

Sequence: 1 SLALDDAFAFRERARLLAERRHWSYMKLLVLDAP 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 187395 seqs, 46645940 residues

Total number of hits satisfying chosen parameters: 187395

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*
1: /cgm2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgm2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgm2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgm2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgm2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgm2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgm2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
8: /cgm2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	196	100.0	39	5	US-09-999-608-160 Sequence 160, Appl
2	196	100.0	39	5	US-09-999-608-168 Sequence 168, Appl
3	55.5	28.3	521	6	US-10-990-328-12930 Sequence 12930, A
4	55.5	28.3	528	6	US-10-990-328-12929 Sequence 12929, A
5	55.5	28.3	528	6	US-10-990-328-12931 Sequence 12931, A
6	55.5	28.3	528	6	US-10-990-328-12934 Sequence 12934, A
7	53	27.0	1078	6	US-10-732-923-4371 Sequence 4371, Ap
8	50	25.5	308	1	PCT-US02-09107B-56061 Sequence 56061, A
9	50	25.5	308	1	PCT-US02-09107B-75211 Sequence 75211, A
10	49.5	25.3	428	1	PCT-US02-09107B-72040 Sequence 72040, A
11	49.5	25.3	558	1	PCT-US02-09107B-63818 Sequence 63818, A

12	49.5	25.3	669	1	PCT-US02-09107B-67679	Sequence 67679, A
13	48.5	24.7	198	8	US-60-613-154-32	Sequence 32, Appl
14	48.5	24.7	330	1	PCT-US02-09107B-67439	Sequence 67439, A
15	48.5	24.7	4442	8	US-60-612-215-23	Sequence 23, Appl
16	48	24.5	239	6	US-10-488-197-69	Sequence 69, Appl
17	48	24.5	389	1	PCT-US02-09107B-75352	Sequence 75352, A
18	48	24.5	389	1	PCT-US02-09107B-76307	Sequence 76307, A
19	48	24.5	389	6	US-10-732-923-11754	Sequence 11754, A
20	48	24.5	389	6	US-10-732-923-11855	Sequence 11855, A
21	48	24.5	389	6	US-10-732-923-11883	Sequence 11883, A
22	48	24.5	554	1	PCT-US02-09107B-62198	Sequence 62198, A
23	48	24.5	585	1	PCT-US02-09107B-66493	Sequence 66493, A
24	48	24.5	591	6	US-10-488-197-71	Sequence 71, Appl
25	48	24.5	1272	1	PCT-US02-09107B-49949	Sequence 49949, A
26	47.5	24.2	161	1	PCT-US02-09107B-48155	Sequence 48155, A
27	47.5	24.2	199	6	US-10-732-923-18516	Sequence 18516, A
28	47	24.0	363	1	PCT-US02-09107B-73133	Sequence 73133, Ap
29	47	24.0	404	6	US-10-408-765-1757	Sequence 1757, Ap
30	47	24.0	553	1	PCT-US02-09107B-53679	Sequence 53679, A
31	47	24.0	1177	6	US-10-732-923-3293	Sequence 3293, Ap
32	46.5	23.7	407	1	PCT-US02-09107B-67671	Sequence 67671, A
33	46.5	23.7	1245	1	PCT-US02-09107B-66632	Sequence 66632, A
34	46.5	23.7	2152	6	US-10-732-923-20632	Sequence 20632, A
35	46	23.5	171	1	PCT-US02-09107B-70053	Sequence 70053, A
36	46	23.5	171	1	PCT-US02-09107B-70053	Sequence 70053, A
37	46	23.5	191	1	PCT-US02-09107B-69327	Sequence 69327, A
38	46	23.5	220	1	PCT-US02-09107B-69327	Sequence 69327, A
39	46	23.5	230	1	PCT-US02-09107B-70162	Sequence 70162, A
40	46	23.5	319	1	PCT-US04-37204-6461	Sequence 6461, Ap
41	46	23.5	326	1	PCT-US02-09107B-44356	Sequence 44356, A
42	46	23.5	525	1	PCT-US02-09107B-78249	Sequence 78249, A
43	46	23.5	531	6	US-10-990-328-12932	Sequence 12932, A
44	46	23.5	531	6	US-10-990-328-12933	Sequence 12933, A
45	46	23.5	549	1	PCT-US02-09107B-62828	Sequence 62828, A

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 15:23:17 ; Search time 39 Seconds
(without alignments)
96.217 Million cell updates/sec

Title: US-10-014-162-1

Perfect score: 196

Sequence: 1 SLALDDAFAFRERARLLAERRHWSYMKLLVLDAP 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*
1: Pirl:*
2: Pirl2:*

3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	58.5	29.8	206	2	C85493	probable DNA repair
2	58.5	29.8	206	2	C90642	Probable DNA repair
3	58.5	29.8	206	2	G64732	yacE protein - Bac
4	58	29.6	611	2	G83177	probable sodium/hy
5	57	29.1	203	2	E83078	conserved hypotet
6	57	29.1	524	1	RGRBAP	nif-specific regul
7	56.5	28.8	206	2	AC0520	conserved hypotet
8	55	28.1	204	2	F72459	hypothetical prote
9	55	28.1	486	2	C96018	probable starch sy
10	53.5	27.3	518	2	S60176	regulatory protein
11	53	27.0	366	2	T42666	hypothetical prote
12	53	27.0	1078	2	T19745	hypothetical prote
13	52.5	26.8	668	2	T02791	mitotic centromere
14	52	26.5	174	2	G83712	hypothetical prote
15	52	26.5	213	2	C82078	hypothetical prote
16	52	26.5	519	1	C25878	conserved hypotet
17	52	26.5	1112	2	T30202	nif-specific regul
18	51.5	26.3	317	2	AD2327	probable chitin sy
19	51.5	26.3	525	2	A10285	hypothetical prote
20	51	26.0	204	2	T08321	transcription regu
21	51	26.0	309	2	AE3325	hypothetical prote
22	51	26.0	414	2	G75832	comL, competence 1
23	51	26.0	572	2	T34345	penicillin-binding
24	51	26.0	605	2	S01066	hypothetical prote
25	50.5	25.8	330	2	H87625	regulatory protein
26	50.5	25.8	522	1	S01927	endo-1,4-beta-xyla
27	50.5	25.8	646	2	AD3409	nif-specific regul
28	50.5	25.8	722	2	F82482	ABC transporter AT
29	50.5	25.8	1852	2	J05546	hypothetical prote
30	50	25.5	174	2	J05035	chitin synthase (E
31	50	25.5	306	2	D70657	propanediol dehydr
32	50	25.5	308	2	AB0524	probable mtr - Myc
33	50	25.5	308	2	S45204	hypothetical ABC t
34	50	25.5	308	2	S45496	probable ABC-type
35	50	25.5	308	2	C90645	hypothetical prote
36	50	25.5	309	2	F75516	hypothetical prote
37	50	25.5	311	2	AC1159	hypothetical prote
38	50	25.5	311	2	AH1516	ABC transporter (A
39	50	25.5	326	2	S54042	hypothetical prote
40	50	25.5	512	2	B83222	regulatory protein
41	50	25.5	715	2	T31097	chitin synthase (E
42	50	25.5	1041	2	T31097	chitin synthase (E
43	50	25.5	1086	2	J06079	chitin synthase (E
44	50	25.5	1195	2	S61886	chitin synthase (E
45	50	25.5	1498	2	S76102	chitin synthase (E

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model
Run on: December 29, 2004, 15:14:41 ; Search time 201 Seconds
(without alignments)

111.640 Million cell updates/sec

Title: US-10-014-162-1
Perfect score: 196
Sequence: 1 SLALADAAFRERARLLAALERRHRLNSYMKLVADAP 39
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing filter: 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	196	100.0	100	2	Q96A98	Q96A98 homo sapien
2	172	87.8	100	2	Q91W27	Q91W27 mus musculu
3	132	67.3	90	2	Q91ZAO	Q91ZAO mus musculu
4	130	66.3	157	2	Q8QGA2	Q8QGA2 brachydanto
5	113	57.7	85	2	Q96DJ4	Q96DJ4 homo sapien
6	70	35.7	603	2	Q9EYV2	Q9EYV2 rhizobium 1
7	69	35.2	607	2	Q9EAV5	Q9EAV5 rhizobium 1
8	60.5	30.9	359	1	FLI_EUCGL	Q9GBX4 eucahyptus
9	60.5	30.9	3579	1	Q8GBX4	Q8GBX4 eucahyptus
10	59.5	30.4	356	2	Q6DV95	Q6DV95 eucahyptus
11	59.5	30.4	493	2	Q6N1N1	Q6N1N1 rhodospneu
12	59.5	30.4	493	2	CAE29815	Q6K8A9 azoarcus sp
13	59	30.1	517	2	Q8KSA9	Q7N811 rhodospneu
14	59	30.1	821	2	Q7N811	Q64953 eucahyptus
15	58.5	29.8	206	1	COAE_ECOL6	Q9GBX4 polypangium
16	58.5	29.8	206	1	COAE_ECOL1	Q6DV95 eucahyptus
17	58.5	29.8	1063	2	Q821D8	Q6N1N1 rhodospneu
18	58.5	29.8	4557	2	Q8CJN6	Q6K8A9 azoarcus sp
19	58	29.6	225	2	Q8STN5	Q7N811 rhodospneu
20	58	29.6	380	2	Q8N1H5	Q64953 eucahyptus
21	58	29.6	467	2	Q6MZY8	Q9GBX4 polypangium
22	58	29.6	467	2	CAE45919	Q6DV95 eucahyptus
23	58	29.6	590	2	Q6P989	Q6N1N1 rhodospneu
24	58	29.6	590	2	Q6KXK1	Q6K8A9 azoarcus sp
25	58	29.6	590	2	Q8N865	Q7N811 rhodospneu
26	58	29.6	590	2	AAH60879	Q64953 eucahyptus
27	58	29.6	611	2	Q9HXO5	Q9GBX4 polypangium
28	57.5	29.3	206	1	COAE_SHIFL	Q6DV95 eucahyptus
29	57.5	29.3	362	2	Q7N1L36	Q6N1N1 rhodospneu
30	57	29.1	203	1	COAE_PSEAE	Q6MZY8 eucahyptus
31	57	29.1	524	1	NIFA_KLB0X	Q6K8A9 azoarcus sp
32	56.5	28.8	206	1	COAE_SALTY	Q6N1N1 rhodospneu
33	56.5	28.8	408	2	Q73WDL	Q6K8A9 azoarcus sp
34	56.5	28.8	408	2	AA505046	Q64953 eucahyptus
35	56.5	28.8	408	2	AA505046	Q64953 eucahyptus

36	56	28.6	588	2	Q9D5Y0	Q945Y0	m mus muscu
37	55.5	28.3	290	2	Q89TF0	Q89tf0	bradyrhi zob
38	55.5	28.3	295	2	Q9AMW7	Q9amw7	bradyrhi zob
39	55.5	28.3	433	2	Q8P4L8	Q8p4l8	xanthomona s
40	55.5	28.3	521	2	Q93JT3	Q93jt3	pseudomona s
41	55.5	28.3	736	2	Q8BLL9	Q8bll9	mus musculu
42	55.5	28.3	737	2	Q8N3E9	Q8n3e9	homo sapien
43	55.5	28.3	757	2	Q8TF37	Q8tf37	homo sapien
44	55.5	28.3	785	2	Q8K2J0	Q8k2j0	mus musculu
45	55.5	28.3	789	2	Q8TEC1	Q8tec1	homo sapien

ALIGNMENTS